AMENDMENTS TO THE SPECIFICATION

Please delete the sequence listing from the published international application and replace with the sequence listing submitted on compact disc enclosed herewith.

In the specification at page 1, after the title and before line 3, please insert the following:

-- RELATED APPLICATIONS

This application is a national stage application (under 35 U.S.C. 371) of PCT/EP2004/008683 filed August 3, 2004 which claims benefit of European patent application 03018266.1 filed August 11, 2003.

SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2) and a computer readable form copy of the Sequence Listing (CRF COPY), all on compact disc, each containing: file name: Final Sequence list-13477-00002-US, date recorded: February 10, 2006, size: 166 KB. --

In the specification at page 72-73, please replace Table 3A with the following amended Table 3A:

Table 3A. Overview of markers used for mapping Rpiblb2

Marker	Ori[1)]	Sequence	SEQ ID NO:	Annealing temp (°C)	Restriction Enzyme[2)]
E46M52	F	TTGTGGTTATCGATGAGAAT	11	56,5	SCAR (b)
	R	GAAACAACAGCAGGATAGTGAG	12		
E46M52e	F	TTGTGGTTATCGATGAGAAT	13	61	SCAR (a,b);MboI (c)
	R	GAAACAACAGCAGGATAGTGAG	14		
E40M58	F	GAATTCAGCACAAATACCAA	15	50	DdeI (a)
	R	TTAACGTTTACTATCACGAG	16		
E40M58e	F	GTAGAAACAGCAGCCTCATAAGC	17	55	SCAR (a)
	R	TTCTGCCTAATTGCCCTGTG	18		
S1E00	F	GGGGTTGGGAAGACAACGACAC	19	50	AFLP
	R	AATTCCAAGATACAGTCAAATAC	20		
41L	F	AGGCAGGATTAACAGTAGAAG	21	58	TaqI (a)
	R	CATGCTTTTAGGAAGAAGCTC	22		
36L	F	TTGAGACAAAGCAGCTCCAC	23	59	ApoI (a,b)
	R	ACGTTTCTCACACCTACAGG	24		
69L	F	TGATGGCACGTTTGATCGTG	25	61	TaqI (a,b);HpaII (c)
	R	TAAGATCCAAACCAGCCACC	26		
69R	F	CCTTATCACACATGTGGCTAC	27	58	RsaI (a,b); ApoI (c)
	R	ATTGAAACGGAGGAAGTACAAC	28		
141R	F	TTCTTCATATGGCAGACCAAC	29	60	RsaI (a,b); DdeI (c)
	R	CTACTCTGCTGACATGCAGG	30		
24L	F	GAGATTCTCAAAGGTGTCTTCC	31	60	SCAR (a,b,c)
	R	AACCTGTGCTTTCCCATTCG	32		
24R	F	CTTTCACAAGCGTCACTTTGG	33	58	SCAR (a,b)
	R	TAAAAAGAATCAACAGGGCAAC	34		
14L	F	ACGACTGCTCAAAGTTGGCC	35	58	SCAR (a,b,c)
	R	CCAAGAAGCCAGTTGAGAGC	36		
123L	F	GTAGATTACACTATGGATATGG	37	60	SCAR (a,b)
	R	CAGTTAGCAGCAATGTCAGC	38		
123L2	F	CATTCAACTAGGCCAAAAGTGG	39	59	SCAR (a,b); DraI (c)
	R	CCAGGTAGGTGTTTTCTTCC	40		
123R	F	GTTCTAAGTCAGATGCCACC	41	62	SCAR (a,b)
	R	AAGTGCTCCAACACGAGCC	42		

133R	F	TGAGTTCTCTTACCCTGCG	43	60	SCAR (a,b)
	R	GGATATCCAGCATCAATGCC	44		
133R2	F	GGTGAGCCTCCTTGCATTCC	45	60	SCAR (a,b)
	R	CCTGAGGGAAGATGTCACG	46		
99L	F	CCTAGTTTAGAGTGAGTAGAC	47	58	SCAR (a,b)
	R	GTGATATATTGCTCAAGGATCC	48		
113R	F	GTTGCTGGCTGTCACTGATC	49	59	SCAR (a,b)
	R	GTGATGTGCAGGGTTCAAGG	50		
67L	F	GATTAGTGTAGATCTTAGCTTG	51	62	MboI (a,b)
	R	AAATCTCTCTCACAATTATCCC	52		
112L	F	CTATTGACTGAACCTGCTGAG	53	56	HaeIII (a); HinfI (c)
	R	TGAAGTCATTTAGTCCACAGC	54		
CT216 (RFLP)	F	AGATCGGAGTGTGAACATGG	55	56	
	R	CTTCTACTTCTAGTCGACTGC	56		
CT216	F	CGTAGTCCATCTGAAGCTCC	57	65	SCAR (a,b)
	R	TCTTCTTCTGCTAGTCGTCG	58		
CT119	F	ACTATTCTCACGTAAGGGGACAC	59	60	HindIII (a,b)
	R	GTGTACATGTATGAAACTCTAGC	60		
CT119N	F	GTTCCTTTCAATCAGAAAGTAG	61	55	SCAR (a)
	R	CTTTGGATGAGTCAAAAGGCT	62		
14L24L	F	univ14L		60	CfoI (c)
	R	univ24L			
SPB30L	F	CAAGTTACGGCAACCAAGAG	63	57	HpaII (c)
	R	CTTTGACACAGTGTTAGAATGC	64		
SPB39L	F	CGTGATCTAGGAGTTACGAC	65	52	SCAR (c)
	R	CTTATTTTAAATACAAGACATCTGG	66		
24L9spec	F	univ. 14L		56	HhaI (c)
	R	CAGAGGAAAGTCAACCAACG	67		
24Lspec	F	univ. 14L		60	CfoI (c)
	R	CAGAGGAAAGTCAACCAACG	68		
NptII	F	TCGGCTATGACTGGGCACAACAGA	69	70	
	R	AAGAAGGCGATAGAAGGCGATGCG	70		
M13	F	TGTAAAACGACGGCCAGT	71	55	
	R	GGAAACAGCTATGACCATG	72		

[1] Ori: Orientation of the primer; F: forward primer; R: reverse primers
[2] a: ARG95-3, b: ARP96-11, c: B6a

In the specification at page 74, please replace Table 3B with the following amended Table 3B:

~~Tabel~~ **Table 3B.** Overview of primers used for mapping Rpi-blb2

primer	Ori	Sequence[1)]	SEQ ID NO:
ARO 73	F	TTCAGCACAAATACCAAT	73
ARO 74	R	GATGTTCCCCTTCTTTTA	74
ARO 77	R	TTGTGGTTATCGATGAGAAT	75
ARO 79	R	ACCTGGCGTTCCTTATTTTT	76
ARO 94		NGTCASWGANAWGAA	77
ARO 128	F	GATGGAGCGGAAAAGCCGGTG	78
ARO 129	F	GGTGTTTTGTAGCATCTCCAG	79
ARO 295		CCATGATTACGCCAAGCTGG	80
ARO 296		GGTTTTCCCAGTCACGACGT	81
univ14L	F	AGAAAGCTCACCAGTGGACC	82
univ24L	R	ATTTATGGCTGCAGAGGACC	83
123Mi	R	AAGTCCAATTGCTCATCCATC	84
14L2	R	TGCACCATGCACGAAGGTC	85
24L2	F	CAATWTTGGTTCCCGAAATTGG	86
ARF1F	F	ATGGAAAAACGAAAAGATAATGAAG	87
ARF1R	R	CTACTTAAATAACGGGATATCCTTC	88
ARO 602	F	CCCATGACTCCTTGAGTTTG	89
S1		GGTGGGGTTGGGAAGACAACG	90
EcoR1+0		GTAGACTGCGTACCAATTC	91
MseI+0		GATGAGTCCTGAGTAA	92
ARO 769		GTGCTTCATTCAAACTCAAGGAG	95
ARO 770		CTGAACTAGAAAAACTCACTGTAGA	96
ARO 771		GTTTGAAAAGATTGCAATTGCATG	97
ARO 772		CTCAGCCATCAGTTGAAACAGAGA	98
ARO 774		GAGAGAGATTCAAGAGGAGGAAGC	99

[1)] N=A+T+G+C, S=G+C,W=A+T

In the specification at page 79 line 21, please replace the paragraph starting with "Figure 13" with the following amended paragraph:

Figure 13. Nucleic acid sequences coding for the Rpi-blb2 gene. **A.** Coding nucleic acid sequence of the Rpi-blb2 gene (SEQ ID NO: 1). **B.** Coding nucleic acid sequence of the Rpi-blb2 gene including the intron sequence (position 43-128) (SEQ ID NO: 3). **C.** Sequence of the 7967 bp Sau3AI genomic DNA fragment of ARD 1197-16 BAC 211 present in p211F-C12 (SEQ ID NO: 5), one of the two ~~the~~ genetic constructs used for genetic complementation for late blight

resistance. The genomic fragment harbours the Rpi-blb2 gene including natural regulatory elements necessary for correct expression of the gene. The initiation codon (ATG position 1546-1548) and the termination codon (TAG position 5433-5435) are underlined. **D.** Sequence of the 9949 bp Sau3AI genomic DNA fragment of S. bulbocastanum 2002 BAC BlbSP39 present in pSP39-20 (SEQ ID NO: 6), one of the two ~~the~~ genetic constructs used for genetic complementation for late blight resistance. The genomic fragment harbours the Rpi-blb2 gene including natural regulatory elements necessary for correct expression of the gene. The initiation codon (ATG position 1413-1415) and the termination codon (TAG position 5300-5303) are underlined.

In the specification at page 79 line 36, please replace the paragraph starting with "Figure 14" with the following amended paragraph:

Figure 14. Putative Rpi-blb2 gene structure and deduced Rpi-blb2 protein sequence. **A.** Schematic representation of the Rpi-blb2 gene structure. Horizontal lines indicate exons. Open boxes represent coding sequence. Lines angled downwards indicate the positions of intron sequences. **B.** Deduced Rpi-blb2 protein sequence (SEQ ID NO: 4). The amino acid sequence deduced from the DNA sequence of Rpi-blb2 is divided into three domains (LZ, NBS and LRR). Hydrophobic residues in domain A that form the first residue of heptad repeats of the potential leucine zipper (LZ) domain are underlined. Conserved motifs in R proteins are written in lowercase and in italic in the NBS domain. Residues matching the consensus of the cytoplasmic LRR are indicated in bold in the LRR domain. Dots in the sequence have been introduced to align the sequence to the consensus LRR sequence of cytoplasmic LRRs.

In the specification at page 80 line 8, please replace the paragraph starting with "Figure 15" with the following amended paragraph:

Figure 15. Alignment of the deduced protein products encoded by Rpi-blb2 (SEQ ID NO: 4), Mi-1.1 (SEQ ID NO: 8) and Mi-1.2 (SEQ ID NO: 10). The complete amino acid sequence of Rpi-blb2 is shown and amino acid residues from Mi-1.1 and Mi-1.2 that differ from the corresponding residue in Rpi-blb2. Dashes indicate gaps inserted to maintain optimal alignment. Amino acid residues that are specific for Rpi-blb2, when compared to those at corresponding

positions in Mi-1.1 and Mi-1.2 are highlighted in bold and red. The regions of the LRRs that correspond to the β-strand/β-turn motif xxLxLxxxx are underlined. Conserved motifs in the NBS domain are indicated in lowercase. A vertical line indicates the division between CC-NBS and LRR region. The position of the VLDL motif which is conserved in the third LRR of many plant R proteins but not in Rpi-blb2 is indicated by a shaded rectangle.

In the specification at page 80 line 19, please replace the paragraph starting with "Figure 16" with the following amended paragraph:

Figure 16. CLUSTAL W (1.82) Multiple Sequence Alignments of Mi1.1 (SEQ ID NO: 7), Mi1.2 (SEQ ID NO: 9) and Rpi-blb2 (SEQ ID NO: 1) nucleic acids.

In the specification at page 80 line 22, please replace the paragraph starting with "Figure 17" with the following amended paragraph:

Figure 17. CLUSTAL W (1.82) Multiple Sequence Alignments of Mi1.1 (SEQ ID NO: 8), Mi1.2 (SEQ ID NO: 10) and Rpi-blb2 (SEQ ID NO: 2) proteins.